AMENDMENTS TO THE SPECIFICATION

Please amend the paragraph beginning on page 30, line 11 as follows.

Any region of the human XIAP IRES may be used as a target for antisense inhibition of XIAP translation, and particular sequences for XIAP IRES antisense nucleic acids may be selected by well-known approaches. For example, if desired, computer algorithms may be used to identify sequences that form the most stable hybridization duplexes. Computer algorithms may also be used to identify regions of the XIAP IRES that are relatively accessible within a folded mRNA molecule; antisense nucleic acids against such regions are more likely to effectively inhibit translation of XIAP mRNA. For example, the sequence at ~~-153 through -139~~ -154 through -140 of the human XIAP IRES DNA sequence (5'-GTTTCTTAGCGGTCG-3'; SEQ ID NO: 7; see Fig. 4) is predicted to be accessible for hybridization within endogenous XIAP mRNA; therefore, an antisense nucleic acid that is complementary this sequence, e.g., 5'-CGACCGCTAAGAAAC-3' (SEQ ID NO: 8) or 5'-CGACCGCUAAGAAAC-3' (SEQ ID NO: 9) is useful for decreasing endogenous XIAP levels, thereby increasing the sensitivity of a target cell to an apoptotic stimulus. Computer algorithms that may be used to identify optimal XIAP IRES sequences for generating antisense nucleic acids include, but are not limited to, OLIGO 5.0 from National Biosciences Inc. ~~(http://www.sxst.it/nbi_olg.htm) and MFOLD (http://mfold2.wustl.edu/~mfold/rna/form1.cgi)~~. References describing algorithms for predicting secondary structure are described in M. Zuker et al. "Algorithms and Thermodynamics for RNA Secondary Structure Prediction: A Practical Guide." in: RNA Biochemistry and Biotechnology, J. Barciszewski & B.F.C. Clark, eds., NATO ASI Series, Kluwer Academic Publishers (1999) and in Mathews et al. *J. Mol. Biol.* 288:911-940 (1999).

Please delete the paragraph beginning on page 53, line 6.